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     (FILE 'HOME' ENTERED AT 13:57:34 ON 01 APR 2002)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 13:57:58 ON 01 APR 2002
L1          5706 S CORYNEBACTERIUM (A)GLUTAMICUM
L2             0 S PHOSPHOENYLPYRUVATE (W)SUGAR (W)PHOSPHOTRANSFERASE?
L3          3480 S "SUGAR PHOSPHOTRANSFERASE?"
L4            11 S PHOSPHOENYLPYRUVATE
L5            16 S L1 AND L3
L6            10 DUP REM L5 (6 DUPLICATES REMOVED)
L7         19911 S "PTS"
L8          1406 S L3 AND L7
L9        152465 S PYRUVATE
L10          146 S L8 AND L9
L11            0 S L1 AND L10
L12        11661 S BREVIBACTERIUM
L13            5 S L12 AND L10
L14            2 DUP REM L13 (3 DUPLICATES REMOVED)
L15          473 S L3 AND "PEP"
L16          280 S L15 AND L7
L17           48 S L9 AND L16
L18           24 DUP REM L17 (24 DUPLICATES REMOVED)
L19            0 S L18 AND L1
                 E POMPEJUS M/AU
L20           26 S E3
L21           48 S E3-E4
                 E KROGER B/AU
L22           92 S E3
                 E SCHRODER H/AU
L23         1910 S E3
                 E ZELDER O/AU
L24          180 S E3
                 E HABERHAUER G/AU
L25          236 S E3-E6
L26         2444 S L21 OR L22 OR L23 OR L24 OR L25
L27            0 S L26 AND L17
L28            2 S L26 AND L3

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NEWS 3 Jan 25 Searching with the P indicator for Preparations
NEWS 4 Jan 29 FSTA has been reloaded and moves to weekly updates
NEWS 5 Feb 01 DKILIT now produced by FIZ Karlsruhe and has a new update frequency
NEWS 6 Feb 19 Access via Tymnet and SprintNet Eliminated Effective 3/31/02
NEWS 7 Mar 08 Gene Names now available in BIOSIS
NEWS 8 Mar 22 TOXLIT no longer available
NEWS 9 Mar 22 TRCTHERMO no longer available
NEWS 10 Mar 28 US Provisional Priorities searched with P in CA/CAplus and USPATFULL
NEWS 11 Mar 28 LIPINSKI/CALC added for property searching in REGISTRY

NEWS EXPRESS February 1 CURRENT WINDOWS VERSION IS V6.0d, CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP), AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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FILE 'HOME' ENTERED AT 13:57:34 ON 01 APR 2002

=> file medline embase biosis biotechds scisearch hcaplus ntis lifesci
COST IN U.S. DOLLARS SINCE FILE ENTRY 0.21 TOTAL SESSION 0.21
FULL ESTIMATED COST

FILE 'MEDLINE' ENTERED AT 13:57:58 ON 01 APR 2002

FILE 'EMBASE' ENTERED AT 13:57:58 ON 01 APR 2002

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FILE 'SCISEARCH' ENTERED AT 13:57:58 ON 01 APR 2002

FILE 'HCAPLUS' ENTERED AT 13:57:58 ON 01 APR 2002

FILE 'NTIS' ENTERED AT 13:57:58 ON 01 APR 2002

FILE 'LIFESCI' ENTERED AT 13:57:58 ON 01 APR 2002


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=> s corynebacterium (a)glutamicum
L1         5706 CORYNEBACTERIUM (A) GLUTAMICUM

=> s phosphoenylpyruvate (w)sugar (w)phosphotransferase?
L2            0 PHOSPHOENYLPYRUVATE (W) SUGAR (W) PHOSPHOTRANSFERASE?

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SEARCH ENDED BY USER

=> s "sugar phosphotransferase?"
L3         3480 "SUGAR PHOSPHOTRANSFERASE?"

=> s phosphoenylpyruvate
L4           11 PHOSPHOENYLPYRUVATE

=> s l1 and l3
L5           16 L1 AND L3

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6           10 DUP REM L5 (6 DUPLICATES REMOVED)

=> d 1-10 ibib ab

L6    ANSWER 1 OF 10  BIOTECHDS COPYRIGHT 2002 DERWENT INFO AND ISI
ACCESSION NUMBER: 2001-04894  BIOTECHDS
TITLE:            Corynebacterium glutamicum nucleic acids
                  encoding phosphoenolpyruvate:sugar
                  phosphotransferase system proteins or their portions,
                  useful for typing or identifying C.  glutamicum or related
                  bacteria, and as markers for transformation;
                     selectable marker
AUTHOR:           Pompejus M; Kroeger B; Schroeder H; Zelder O; Haberhauer G
PATENT ASSIGNEE:  BASF
LOCATION:         Ludwigshafen, Germany.
PATENT INFO:      WO 2001002583 11 Jan 2001
APPLICATION INFO: WO 2000-DE973 27 Jun 2000
PRIORITY INFO:    DE 1999-1042097 3 Sep 1999; US 1999-142691 1 Jul 1999
DOCUMENT TYPE:    Patent
LANGUAGE:         English
OTHER SOURCE:     WPI: 2001-080989 [09]
AB    Isolated Corynebacterium glutamicum ATCC 13032
      nucleic acids encoding phosphoenolpyruvate:sugar-
      phosphotransferase system (PTS) proteins or their fragments are
      claimed.  A PTS nucleic acid (N1) does not consist of any of the
      F-designated genes defined and is selected from one of 17 disclosed
      nucleic acid sequences (S1) and their fragments nucleic acid which encode
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a protein selected from one of the 17 protein sequences (S2) disclosed; nucleic acid encoding a naturally occurring allelic variant of a protein selected from (S2). Also claimed are methods for producing the proteins; C. glutamicum PTS protein and its fragments; diagnosis of Corynebacterium diphtheriae infection; fusion proteins; antisense PTS nucleic acid; a method for screening molecules which modulate the activity of a PTS protein; and a transformed host cell. (144pp)

L6 ANSWER 2 OF 10 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:31659 HCAPLUS
DOCUMENT NUMBER: 134:96287
TITLE: **Corynebacterium glutamicum** genes encoding phosphoenolpyruvate:**sugar phosphotransferase** system proteins
INVENTOR(S): Pompejus, Markus; Kroger, Burkhard; Schroder, Hartwig; Zelder, Oskar; Haberhauer, Gregor
PATENT ASSIGNEE(S): BASF Aktiengesellschaft, Germany
SOURCE: PCT Int. Appl., 143 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001002583	A2	20010111	WO 2000-IB973	20000627
WO 2001002583	A3	20010726		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:
US 1999-142691P P 19990701
US 1999-150310P P 19990823
DE 1999-19942095 A 19990903
DE 1999-19942097 A 19990903

AB Isolated nucleic acid mols., designated phosphoenolpyruvate:**sugar phosphotransferase** (PTS) nucleic acid mols., which encode novel PTS proteins from **Corynebacterium glutamicum** are described. The invention also provides antisense nucleic acid mols., recombinant expression vectors contg. PTS nucleic acid mols., and host cells into which the expression vectors have been introduced. The invention still further provides isolated PTS proteins, mutated PTS proteins, fusion proteins, antigenic peptides and methods for the improvement of prodn. of a desired compd. from C. glutamicum based on genetic engineering of PTS genes in this organism.

L6 ANSWER 3 OF 10 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2001700841 MEDLINE
DOCUMENT NUMBER: 21617011 PubMed ID: 11741338
TITLE: The ptsI gene encoding enzyme I of the phosphotransferase system of **Corynebacterium glutamicum**.
AUTHOR: Kotrba P; Inui M; Yukawa H
CORPORATE SOURCE: Research Institute of Innovative Technology for the Earth, 9-2, Kizugawadai, Kizu-cho, Soraku-gun, Kyoto, 619-0292, Japan.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001

Dec 21) 289 (5) 1307-13.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011220
Last Updated on STN: 20020220
Entered Medline: 20020219

AB The phosphoenolpyruvate:carbohydrate phosphotransferase system (PTS) is widespread among bacteria where it mediates carbohydrate uptake and often serves in carbon control. Here we present cloning and analysis of the monocistronic ptsI gene of **Corynebacterium glutamicum** R, which encodes PTS Enzyme I (EI). EI catalyzes the first reaction of PTS and the reported ptsI was shown to complement the corresponding defect in Escherichia coli. The deduced 59.2-kDa EI of 564 amino acids shares more than 50% homology with EIs from Bacillus stearothermophilus, Bacillus subtilis, and Lactobacillus sake. Chromosomal inactivation of ptsI demonstrated that EI plays an indispensable role in PTS of C. glutamicum R and this system represents a dominant sugar uptake system. Cellobiose was only transported and utilized in adaptive mutants of C. glutamicum R. Cellobiose transport was also found to be PTS-dependent and repressed by PTS sugar glucose.

L6 ANSWER 4 OF 10 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001274434 MEDLINE
DOCUMENT NUMBER: 21258526 PubMed ID: 11361073
TITLE: **Corynebacterium glutamicum**: a dissection of the PTS.
AUTHOR: Parche S; Burkovski A; Sprenger G A; Weil B; Kramer R; Titgemeyer F
CORPORATE SOURCE: Lehrstuhl fur Mikrobiologie, Friedrich-Alexander-Universitat Erlangen-Nurnberg, Germany.
SOURCE: JOURNAL OF MOLECULAR MICROBIOLOGY AND BIOTECHNOLOGY, (2001 Jul) 3 (3) 423-8.
Journal code: DSF; 100892561. ISSN: 1464-1801.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20011022
Last Updated on STN: 20011022
Entered Medline: 20011018

AB The high-GC Gram-positive actinomycete **Corynebacterium glutamicum** is commercially exploited as a producer of amino acids that are used as animal feed additives and flavor enhancers. Despite its beneficial role, carbon metabolism and its possible influence on amino acid metabolism is poorly understood. We have addressed this issue by analyzing the phosphotransferase system (PTS), which in many bacteria controls the flux of nutrients and therefore regulates carbon metabolism. The general PTS phosphotransferases enzyme I (EI) and HPr were characterized by demonstration of PEP-dependent phosphotransferase activity. An EI mutant exhibited a pleiotropic negative phenotype in carbon utilization. The role of the PTS as a major sugar uptake system was further demonstrated by the finding that glucose and fructose negative mutants were deficient in the respective enzyme II PTS permease activities. These carbon sources also caused repression of glutamate uptake, which suggests an involvement of the PTS in carbon regulation. The observation that no HPr kinase/phosphatase could be detected suggests that the mechanism of carbon regulation in C. glutamicum is different to the

one found in low-GC Gram-positive bacteria.

L6 ANSWER 5 OF 10 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 3
ACCESSION NUMBER: 2000015847 EMBASE
TITLE: Cloning, nucleotide sequencing, and characterization of the ptsG gene encoding glucose-specific enzyme II of the phosphotransferase system from Brevibacterium lactofermentum.
AUTHOR: Yoon K.-H.; Lee K.-N.; Lee J.-K.; Park S.C.
CORPORATE SOURCE: K.-H. Yoon, School of Food Biotechnology, Woosong University, San 7-6, Jayang-Dong, Dong-Gu, Taejon 300-100, Korea, Republic of. ykh@lion.woosong.ac.kr
SOURCE: Journal of Microbiology and Biotechnology, (1999) 9/5 (582-588).
Refs: 31
ISSN: 1017-7825 CODEN: JOMBES
COUNTRY: Korea, Republic of
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A Brevibacterium lactofermentum gene coding for a glucose-specific permease of the phosphoenolpyruvate-dependent phosphotransferase system (PTS) was cloned, by complementing an Escherichia coli mutation affecting a ptsG gene with the B. lactofermentum genomic library, and completely sequenced. The gene was identified as a ptsG, which enables an E. coli transformant to transport non-metabolizable glucose analogue 2-deoxyglucose (2DG). The ptsG gene of B. lactofermentum consists of an open reading frame, of 2,025 nucleotides encoding a polypeptide of 674 amino acid residues and a TAA stop codon. The 3' flanking region contains two stem-loop structures which may be involved in transcriptional termination. The deduced amino acid sequence of the B. lactofermentum enzyme II(Glc) specific to glucose (EII(Glc)) has a high homology with the **Corynebacterium glutamicum** enzyme II(Man) specific to glucose and mannose (EII(Man)), and the Brevibacterium ammoniagenes enzyme II(Glc) specific to glucose (EII(Glc)). The 171-amino-acid C-terminal sequence of the EII(Glc) is also similar to the Escherichia coli enzyme IIA(Glc) specific to glucose (IIA(Glc)). It is interesting that the arrangement of the structural domains, IIBCA, of the B. lactofermentum EII(Glc) protein is identical to that of EIIs specific to sucrose or .beta.- glucoside. Several in vivo complementation studies indicated that the B. lactofermentum EII(Glc) protein could replace both EII(Glc) and EIIA(Glc) in an E. coli ptsG mutant or crr mutant, respectively.

L6 ANSWER 6 OF 10 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:714378 HCAPLUS
DOCUMENT NUMBER: 130:109230
TITLE: L-Lysine experimental yields by **Corynebacterium glutamicum** on carbon substrates
AUTHOR(S): Ruklisha, M.; Ionina, R.
CORPORATE SOURCE: Institute of Microbiology and Biotechnology, University of Latvia, Riga, LV-1586, Latvia
SOURCE: Meded. - Fac. Landbouwkd. Toegepaste Biol. Wet. (Univ. Gent) (1998), 63(4a), 1341-1344
CODEN: MFLBER; ISSN: 1373-7503
PUBLISHER: Universiteit Gent, Faculteit Landbouwkundige en Toegepaste Biologische Wetenschappen
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Growth of C. glutamicum and C. flavum on different carbon and energy substrates was investigated to det. the advantages of definitive

substrates for increasing lysine prodn. and to identify rate-limiting metabolic steps. The impact of the C source on the growth rate, sugar uptake, lysine yield, and catabolic and lysine-synthesizing enzyme activities was detd. Sucrose was the best C source for increased lysine prodn; an equimolar mix. of glucose and fructose was effective also. The obsd. metabolic differences resulted in differences in metabolite overflow in the direction of lysine synthesis.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 7 OF 10 MEDLINE
ACCESSION NUMBER: 1998314508 MEDLINE
DOCUMENT NUMBER: 98314508 PubMed ID: 9652400
TITLE: Carbon-flux distribution in the central metabolic pathways of **Corynebacterium glutamicum** during growth on fructose.
AUTHOR: Dominguez H; Rollin C; Guyonvarch A; Guerquin-Kern J L; Cocaign-Bousquet M; Lindley N D
CORPORATE SOURCE: Centre de Bioingenierie Gilbert Durand, UMR CNRS/INSA & L.A. INRA, Institut National des Sciences Appliquees, Complexe Scientifique de Rangueil, Toulouse, France.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1998 May 15) 254 (1) 96-102.
Journal code: EMZ; 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980811
Last Updated on STN: 19990129
Entered Medline: 19980728

AB Growth of **Corynebacterium glutamicum** on fructose was significantly less than that obtained on glucose, despite similar rates of substrate uptake. This was in part due to the production of overflow metabolites (dihydroxyacetone and lactate) but also to the increased production of CO2 during growth on fructose. These differences in carbon-metabolite accumulation are indicative of a different pattern of carbon-flux distribution through the central metabolic pathways. Growth on glucose has been previously shown to involve a high flux (> 50% of total glucose consumption) via the pentose pathway to generate anabolic reducing equivalents. NMR analysis of carbon-isotope distribution patterns of the glutamate pool after growth on 1-13C- or 6-13C-enriched fructose indicates that the contribution of the pentose pathway is significantly diminished during exponential growth on fructose with glycolysis being the predominant pathway (80% of total fructose consumption). The increased flux through glycolysis during growth on fructose is associated with an increased NADH/NAD+ ratio susceptible to inhibit both glyceraldehyde-3-phosphate dehydrogenase and pyruvate dehydrogenase, and provoking the overflow of metabolites derived from the substrates of these two enzymes. The biomass yield observed experimentally is higher than can be estimated from the apparent quantity of NADPH associated with the pentose pathway and the flux through isocitrate dehydrogenase, suggesting an additional reaction yielding NADPH. This may involve a modified tricarboxylic acid cycle involving malic enzyme, expressed to significantly higher levels during growth on fructose than on glucose, and a pyruvate carboxylating anaplerotic enzyme.

L6 ANSWER 8 OF 10 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:184754 HCAPLUS
DOCUMENT NUMBER: 128:292608
TITLE: Determination of the carbon flux in the central

metabolism of **Corynebacterium glutamicum** by 13C-isotope analysis

AUTHOR(S): Marx, Achim

CORPORATE SOURCE: Inst. Biotechnologie, Forschungszentrum Juelich G.m.b.H., Juelich, D-52425, Germany

SOURCE: Ber. Forschungszent. Juelich (1997), Juel-3459, 1-111 pp.
CODEN: FJBEE5; ISSN: 0366-0885

DOCUMENT TYPE: Report

LANGUAGE: German

AB All C fluxes of the central metab. of C. glutamicum were quantified and the role and coordination of single metabolic pathways were studied under different metabolic situations. A method based on 13C-data was established to quantify all metabolite fluxes of the central metab. Strong sensitivities were indicated between metabolic fluxes and 13C data, thus allowing the detn. of metabolite flux. When the 13C-content of the position oxalacetate C-4 was varied by the factor 2 it could be shown if anaplerotic prodn. of C4-bodies was via the carboxylation of C3-bodies or via the glyoxalate cycle. A hyperbolic relationship was shown for the bi-directional turnover of transketolase and the 13C-content of the position pentose-5-phosphate C-1 and for the bi-directional metabolite flux between C3-bodies of glycolysis and C4-bodies of the tricarboxylate (TCA) cycle and 13C-enrichment of the position oxalacetate C-2. The NADPH balance showed that, depending on the conditions, more NADPH was produced than necessary for the synthesis of biomass and products. The NADPH excess was 16-67% in relation to the glucose uptake rate. Depending on the metabolic situation, the C4-body-decarboxylation was 10-132% and opposed to the carboxylation of C3-bodies for the anaplerotic supply of the TCA cycle. C4-body-decarboxylation and NADPH-excess as adaptations to high prodn. of Lys were minimal, with a yield coeff. of 0.32 molLysmolglucose-1. The contribution of malate enzyme to a total NADPH prodn. of 211% was small. The pentose phosphate pathway (PPP) and the TCA cycle produced 3/4 and 1/4, resp., of the total NADPH. Overexpression of glutamate dehydrogenase in a mutant of strain MH20-22B resulted in low TCA cycle flux and a high metabolite flux through the oxidative PPP. A high TCA cycle flux was detected during glutamate prodn. using strain LE4. The PPP flux was low in this strain. In a mutant of strain MH20-22B producing Lys and using NADH for synthesis of glutamate, TCA cycle flux was 79% and that of PPP was 26%. The low PPP was due to low NADPH consumption and high NADPH prodn. from isocitrate dehydrogenase of the TCA cycle. A strain ATCC 13032 isocitrate dehydrogenase mutant with a blocked TCA cycle showed a PPP flux of 62%. This mutant showed a glyoxalate cycle active in vivo when metabolizing glucose. This metabolite flux was 53%. A flux of 16% produced anaplerotically C4-bodies. At a flux of 37% the glyoxalate cycle released CO2 by C4-body decarboxylation and pyruvate dehydrogenase.

L6 ANSWER 9 OF 10 MEDLINE DUPLICATE 4

ACCESSION NUMBER: 94314161 MEDLINE

DOCUMENT NUMBER: 94314161 PubMed ID: 8039653

TITLE: Nucleotide sequence of the gene encoding the **Corynebacterium glutamicum** mannose enzyme II and analyses of the deduced protein sequence.

AUTHOR: Lee J K; Sung M H; Yoon K H; Yu J H; Oh T K

CORPORATE SOURCE: Genetic Engineering Research Institute, Korea Institute of Science and Technology, Yusung, Taejon, South Korea.

SOURCE: FEMS MICROBIOLOGY LETTERS, (1994 Jun 1) 119 (1-2) 137-45.
Journal code: FML; 7705721. ISSN: 0378-1097.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-L18874

ENTRY MONTH: 199408
ENTRY DATE: Entered STN: 19940905
Last Updated on STN: 19940905
Entered Medline: 19940825

AB The complete nucleotide sequence of the gene encoding the **Corynebacterium glutamicum** mannose enzyme II (EIIMan) was determined. The gene consisted of 2052 base pairs encoding a protein of 683 amino acid residues; the molecular mass of the protein subunit was calculated to be 72570 Da. The N-terminal hydrophilic domain of EIIMan showed 39.7% homology with a C-terminal hydrophilic domain of Escherichia coli glucose-specific enzyme II (EIIGlc). Similar homology was shown between the C-terminal sequence of EIIMan and the E. coli glucose-specific enzyme III (EIIIGlc), or the EIII-like domain of Streptococcus mutans sucrose-specific enzyme II. Sequence comparison with other EIIs showed that EIIMan contained residues His-602 and Cys-28 which were homologous to the potential phosphorylation sites of EIIIGlc, or EIII-like domains, and hydrophilic domains (IIB) of several EIIs, respectively.

L6 ANSWER 10 OF 10 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1993:482699 BIOSIS
DOCUMENT NUMBER: PREV199396116299
TITLE: Characterization of phosphoenolpyruvate carboxykinase from **Corynebacterium glutamicum**.
AUTHOR(S): Jetten, Mike S. M. (1); Sinskey, Anthony J.
CORPORATE SOURCE: (1) Dep. Biol., Room 16-238, Mass. Inst. Technol., 77 Massachusetts Ave., Cambridge, MA 02139 USA
SOURCE: FEMS (Federation of European Microbiological Societies) Microbiology Letters, (1993) Vol. 111, No. 2-3, pp. 183-188.
ISSN: 0378-1097.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Phosphoenolpyruvate (PEP) carboxykinase is present in crude extracts of **Corynebacterium glutamicum** grown on both glucose and lactate. Preparation of PEP carboxykinase free from interfering PEP carboxylase and oxaloacetate decarboxylase showed an absolute dependence on divalent manganese and IDP for activity in the oxaloacetate (OAA) formation. Other diphosphate nucleotides could not substitute for IDP. The enzyme activity displayed Michaelis-Menten kinetics for the substrates PEP, IDP, KHCO-3, OAA and ITP with a K-m of 0.7 mM, 0.4 mM, 12 mM, 1.0 mM, and 0.5 mM, respectively. At the optimum pH of 6.6, 850 nmol of OAA were formed per min per mg of protein. ATP inhibited PEP carboxykinase in the OAA forming reaction for 60% at 0.1 mM, indicating that the enzyme mainly functions in gluconeogenesis.

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=> s "PTS"
L7       19911 "PTS"

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     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 13:57:58 ON 01 APR 2002
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L5           16 S L1 AND L3
L6           10 DUP REM L5 (6 DUPLICATES REMOVED)
L7        19911 S "PTS"
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L8        1406 L3 AND L7

=> s pyruvate
L9      152465 PYRUVATE

=> s l8 and l9
L10        146 L8 AND L9

=> s l1 and l10
L11          0 L1 AND L10

=> s brevibacteriumkj
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=> s brevibacterium
L12      11661 BREVIBACTERIUM

=> s l12 and l10
L13          5 L12 AND L10

=> dup rem l13
PROCESSING COMPLETED FOR L13
L14          2 DUP REM L13 (3 DUPLICATES REMOVED)

=> d 1-2 ibib ab

L14  ANSWER 1 OF 2  LIFESCI    COPYRIGHT 2002 CSA
ACCESSION NUMBER:   87:51976  LIFESCI
TITLE:              Phosphoenol-pyruvate:sugar
                    phosphotransferase systems and sugar metabolism in
                    Brevibacterium flavum .
AUTHOR:             Mori, M.; Shiio, I.
CORPORATE SOURCE:   Cent. Res. Lab., Ajinomoto Co., Ltd., Kawasaki-ku,
                    Kawasaki, Kanagawa 210, Japan
SOURCE:             AGRIC. BIOL. CHEM., (1987) vol. 51, no. 10, pp. 2671-2678.
DOCUMENT TYPE:      Journal
FILE SEGMENT:       J
LANGUAGE:           English
SUMMARY LANGUAGE:   English
AB   Brevibacterium flavum  mutants defective in the
     phosphoenolpyruvate (PEP)-dependent glucose phosphotransferase system (
     PTS) were selected with high frequency by 2-deoxyglucose-
     resistance. Most of them (DOG super(r)) still had the fructose-PTS
     and grew not only on fructose but also on glucose like the wild-type
     strain. A mutant having 1/8th the fructose-PTS activity of the
     wild strain but normal glucose-PTS activity was isolated as a
     xylitol-resistant mutant. It grew on glucose but not on fructose. The
     glucose-PTS was active on glucose, glucosamine, 2-deoxyglucose
     and mannose, and slightly on methyl- alpha -glucoside and
     N-acetylglucosamine, but not on fructose or xylitol. The fructose-
     PTS acted on fructose and xylitol, and to some extent on glucose
     but not on glucosamine or 2-deoxyglucose. Mutants unable to grow on
     glucose (DOG super(r)Glc super(-)) derived from a DOG super(r) mutant were
     all defective in the fructose-PTS.

L14  ANSWER 2 OF 2  BIOSIS  COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
ACCESSION NUMBER:   1987:277727  BIOSIS
DOCUMENT NUMBER:    BA84:18766
```

TITLE: **PYRUVATE** FORMATION AND SUGAR METABOLISM IN AN AMINO ACID-PRODUCING BACTERIUM **BREVIBACTERIUM** -FLAVUM.
AUTHOR(S): MORI M; SHIIO I
CORPORATE SOURCE: CENT. RES. LAB., AJINOMOTO CO. INC., KAWASAKI-KU, KAWASAKI, KANAGAWA 210, JPN.
SOURCE: AGRIC BIOL CHEM, (1987) 51 (1), 129-138.
CODEN: ABCHA6. ISSN: 0002-1369.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB A **Brevibacterium** flavum mutant lacking **pyruvate** kinase, No. 70, grew on glucose, fructose and sucrose as well as the original wild strain did, but was unable to grow on ribose or gluconate unless **pyruvate** was added. Mutants that required **pyruvate** for growth on ribose were derived directly from the wild strain. Many of them were completely or partially defective in **pyruvate** kinase activity. These **pyruvate** kinase mutants were also unable to grow on gluconate. A phosphoenolpyruvate (PEP): **sugar phosphotransferase** system (**PTS**) was found in B. flavum, which catalyzed the formation of **pyruvate** and sugar phosphate from PEP and sugar. The system required Mg2+, acted on glucose, fructose, mannose, glucosamine and 2-deoxyglucose, and existed in the cells grown on any of the carbon sources tested. Cells grown on fructose, mannitol and sucrose, however, exhibited higher **PTS** activities on fructose than those grown on others. Glucose **PTS** activity was about 20-fold stronger than that of glucokinase. Other sugar metabolic enzymes, inducible mannitol dehydrogenase, gluconokinase, ribokinase and maltase, as well as constitutive invertase were also detected. Oxaloacetate decarboxylase and malic enzyme, which also catalyzed the **pyruvate** formation, were found in B. flavum, but the latter activity was very low in cells grown on glucose. The levels of these enzymes in **pyruvate** kinase mutants unable to grow on ribose or gluconate derived from the wild strain were almost identical to those in the wild-type strain.

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=> d his

     (FILE 'HOME' ENTERED AT 13:57:34 ON 01 APR 2002)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 13:57:58 ON 01 APR 2002
L1          5706 S CORYNEBACTERIUM (A)GLUTAMICUM
L2             0 S PHOSPHOENYLPYRUVATE (W)SUGAR (W)PHOSPHOTRANSFERASE?
L3          3480 S "SUGAR PHOSPHOTRANSFERASE?"
L4            11 S PHOSPHOENYLPYRUVATE
L5            16 S L1 AND L3
L6            10 DUP REM L5 (6 DUPLICATES REMOVED)
L7         19911 S "PTS"
L8          1406 S L3 AND L7
L9        152465 S PYRUVATE
L10          146 S L8 AND L9
L11            0 S L1 AND L10
L12        11661 S BREVIBACTERIUM
L13            5 S L12 AND L10
L14            2 DUP REM L13 (3 DUPLICATES REMOVED)

=> s l3 and "pep"
L15          473 L3 AND "PEP"

=> s l15 and l7
L16          280 L15 AND L7
```

=> s l9 and l16
L17 48 L9 AND L16

=> dup rem l17
PROCESSING COMPLETED FOR L17
L18 24 DUP REM L17 (24 DUPLICATES REMOVED)

=> d 1-24 ibib ab

L18 ANSWER 1 OF 24 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 2002:120013 SCISEARCH
THE GENUINE ARTICLE: 517LH
TITLE: Enzyme I: The gateway to the bacterial phosphoenolpyruvate: **Sugar phosphotransferase** system
AUTHOR: Ginsburg A (Reprint); Peterkofsky A
CORPORATE SOURCE: NHLBI, Biochem Lab, Sect Prot Chem, NIH, Bldg 50, Room 2339, MSC-8012, Bethesda, MD 20892 USA (Reprint); NHLBI, Biochem Lab, Sect Prot Chem, NIH, Bethesda, MD 20892 USA; NHLBI, Cell Biol Lab, NIH, Bethesda, MD 20892 USA
COUNTRY OF AUTHOR: USA
SOURCE: ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (15 JAN 2002) Vol. 397, No. 2, pp. 273-278.
Publisher: ACADEMIC PRESS INC, 525 B ST, STE 1900, SAN DIEGO, CA 92101-4495 USA.
ISSN: 0003-9861.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 38
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Regulatory aspects of the bacterial phosphoenolpyruvate (**PEP**):**sugar phosphotransferase** system (**PTS**) are reviewed. The structure and conformational stability of the first protein (enzyme I) of the **PTS**, as well as the requirement for enzyme I to dimerize for autophosphorylation by **PEP** in the presence of MgCl2 are discussed. (C) 2001 Elsevier Science.

L18 ANSWER 2 OF 24 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:64731 HCAPLUS
DOCUMENT NUMBER: 134:248532
TITLE: Evidence of multiple regulatory functions for the PtsN (IIANtr) protein of Pseudomonas putida
AUTHOR(S): Cases, Ildefonso; Lopez, Juan-Antonio; Albar, Juan-Pablo; De Lorenzo, Victor
CORPORATE SOURCE: Centro Nacional de Biotecnologia CSIC, Madrid, 28049, Spain
SOURCE: Journal of Bacteriology (2001), 183(3), 1032-1037
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The ptsN gene of Pseudomonas putida encodes IIANtr, a protein of the phosphoenol **pyruvate:sugar phosphotransferase** (**PTS**) system which is required for the C source inhibition of the .sigma.54-dependent promoter Pu of the TOL (toluate degrdn.) plasmid pWW0. Using two-dimensional gel electrophoresis, we have examd. the effect of ptsN disruption on the general expression pattern of P. putida. To this end, cells were grown in the presence or absence of glucose, and a 1,117-spot subset of the P. putida proteome was used as a ref. for comparisons. Among all gene products whose expression was lowered by this carbon source (247 spots [about 22%]), only 6 behaved as Pu (i.e., were

depressed in the ptsN background). This evidenced only a minor role for IIANtr in the extensive inhibition of gene expression in P. putida caused by glucose. However, the same expts. revealed a large incidence of glucose-independent effects brought about by the ptsN mutation. As many as 108 spots (ca. 9% of the cell products analyzed) were influenced, pos. or neg., by the loss of IIANtr. By matching this pattern with that of an rpoN::.OMEGA.Km strain of P. putida, which lacks the .sigma.54 protein, we judge that most proteins whose expression was affected by ptsN were unrelated to the alternative sigma factor. These data suggest a role of IIANtr as a general regulator, independent of the presence of repressive carbon sources and not limited to .sigma.54-dependent genes.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 3 OF 24 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2000202048 MEDLINE
DOCUMENT NUMBER: 20202048 PubMed ID: 10736161
TITLE: Enzyme I of the phosphoenolpyruvate:**sugar phosphotransferase** system. In vitro intragenic complementation: the roles of Arg126 in phosphoryl transfer and the C-terminal domain in dimerization.
AUTHOR: Brokx S J; Talbot J; Georges F; Waygood E B
CORPORATE SOURCE: Department of Biochemistry, Health Science Building, University of Saskatchewan, Canada.
SOURCE: BIOCHEMISTRY, (2000 Apr 4) 39 (13) 3624-35.
Journal code: A0G; 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000512
Last Updated on STN: 20000512
Entered Medline: 20000428

AB Enzyme I mutants of the Salmonella typhimurium phosphoenolpyruvate: **sugar phosphotransferase** system (**PTS**), which show in vitro intragenic complementation, have been identified as Arg126Cys (strain SB1690 ptsI34), Gly356Ser (strain SB1681 ptsI16), and Arg375Cys (strain SB1476 ptsI17). The mutation Arg126Cys is in the N-terminal HPr-binding domain, and complements Gly356Ser and Arg375Cys enzyme I mutations located in the C-terminal phosphoenolpyruvate(**PEP**)-binding domain. Complementation results in the formation of unstable heterodimers. None of the mutations alters the K(m) for HPr, which is phosphorylated by enzyme I. Arg126 is a conserved residue; the Arg126Cys mutation gives a V(max) of 0.04% wild-type, establishing a role in phosphoryl transfer. The Gly356Ser and Arg375Cys mutations reduce enzyme I V(max) to 4 and 2%, respectively, and for both, the **PEP** K(m) is increased from 0.1 to 3 mM. It is concluded that this activity was from the monomer, rather than the dimer normally found in assays of wild-type. In the presence of Arg126Cys enzyme, V(max) for Gly356Ser and Arg375Cys enzymes I increased 6- and 2-fold, respectively; the K(m) for **PEP** decreased to <10 &mgr;M, but the K(m) became dependent upon the stability of the heterodimer in the assay. Gly356 is conserved in enzyme I and **pyruvate** phosphate dikinase, which is a homologue of enzyme I, and this residue is part of a conserved sequence in the subunit interaction site. Gly356Ser mutation impairs enzyme I dimerization. The mutation Arg375Cys also impairs dimerization, but the equivalent residue in **pyruvate** phosphate dikinase is not associated with the subunit interaction site. A 37 000 Da, C-terminal domain of enzyme I has been expressed and purified; it dimerizes and complements Gly356Ser and Arg375Cys enzymes I proving that the association/dissociation properties of enzyme I are a function of the

C-terminal domain.

L18 ANSWER 4 OF 24 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:262337 HCAPLUS
DOCUMENT NUMBER: 133:116249
TITLE: ADP Modulates the Dynamic Behavior of the Glycolytic Pathway of Escherichia coli
AUTHOR(S): Diaz Ricci, Juan C.
CORPORATE SOURCE: Departamento de Bioquimica de la Nutricion, Instituto Superior de Investigaciones Biologicas (CONICET-UNT), Instituto de Quimica Biologica "Dr. Bernabe Bloj," Facultad de Bioquimica, Quimica y Farmacia, Universidad Nacional de Tucuman, Tucuman, 4000, Argent.
SOURCE: Biochemical and Biophysical Research Communications (2000), 271(1), 244-249
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A math. model that includes biochem. interactions among the **PTS** system, phosphofructokinase (PFK), and **pyruvate** kinase (PK) is used to evaluate the dynamic behavior of the glycolytic pathway of Escherichia coli under steady-state conditions. The influence of ADP, phosphoenolpyruvate (**PEP**), and fructose-6-phosphate (F6P) on the dynamic regulation of this pathway is also analyzed. The model shows that the dynamic behavior of the system is affected significantly depending on whether ADP, **PEP**, or F6P is considered const. at steady state. Sustained oscillations are obsd. only when dADP/dt .noteq. 0 and completely suppressed if dADP/dt = 0 at any steady-state value. However, when **PEP** or F6P is const., the system evolves toward the formation of stable limit cycles with periods ranging from 0.2 min to hours. (c) 2000 Academic Press.
REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 5 OF 24 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 1999042176 MEDLINE
DOCUMENT NUMBER: 99042176 PubMed ID: 9822815
TITLE: Inducer exclusion in Escherichia coli by non-**PTS** substrates: the role of the **PEP** to **pyruvate** ratio in determining the phosphorylation state of enzyme IIAGlc.
AUTHOR: Hogema B M; Arents J C; Bader R; Eijkemans K; Yoshida H; Takahashi H; Aiba H; Postma P W
CORPORATE SOURCE: E.C. Slater Institute, BioCentrum, University of Amsterdam, Plantage Muidergracht 12, 1018 TV Amsterdam, The Netherlands.
SOURCE: MOLECULAR MICROBIOLOGY, (1998 Nov) 30 (3) 487-98.
Journal code: MOM; 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199901
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19990104
AB The main mechanism causing catabolite repression in Escherichia coli is the dephosphorylation of enzyme IIAGlc, one of the enzymes of the phosphoenolpyruvate:carbohydrate phosphotransferase system (**PTS**). The **PTS** is involved in the uptake of a large number of

carbohydrates that are phosphorylated during transport, phosphoenolpyruvate (**PEP**) being the phosphoryl donor. Dephosphorylation of enzyme IIAGlc causes inhibition of uptake of a number of non-**PTS** carbon sources, a process called inducer exclusion. In this paper, we show that dephosphorylation of enzyme IIAGlc is not only caused by the transport of **PTS** carbohydrates, as has always been thought, and that an additional mechanism causing dephosphorylation exists. Direct monitoring of the phosphorylation state of enzyme IIAGlc also showed that many carbohydrates that are not transported by the **PTS** caused dephosphorylation during growth. In the case of glucose 6-phosphate, it was shown that transport and the first metabolic step are not involved in the dephosphorylation of enzyme IIAGlc, but that later steps in the glycolysis are essential. Evidence is provided that the [**PEP**]-[**pyruvate**] ratio, the driving force for the phosphorylation of the **PTS** proteins, determines the phosphorylation state of enzyme IIAGlc. The implications of these new findings for our view on catabolite repression and inducer exclusion are discussed.

L18 ANSWER 6 OF 24 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:393650 HCAPLUS
DOCUMENT NUMBER: 129:158337
TITLE: Identification of peptides inhibiting enzyme I of the bacterial phosphotransferase system using combinatorial cellulose-bound peptide libraries
AUTHOR(S): Mukhija, Seema; Germeroth, Lothar; Schneider-Mergener, Jens; Erni, Bemhard
CORPORATE SOURCE: Departement fur Chemie und Biochemie, Universitat Bern, Bern, Switz.
SOURCE: Eur. J. Biochem. (1998), 254(2), 433-438
CODEN: EJBCAI; ISSN: 0014-2956
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The phosphoenolpyruvate(P-**pyruvate**)-dependent **sugar phosphotransferase** system (**PTS**) is a transport and signal-transduction system which is almost ubiquitous in bacteria but does not occur in eukaryotes. It catalyzes the uptake and phosphorylation of carbohydrates and is involved in signal transduction, e.g. catabolite repression, chemotaxis, and allosteric regulation of metabolic enzymes and transporters. EI (Enzyme I of the **PTS**) is the first and central component of the divergent **PTS** (P-**pyruvate**-dependent **sugar phosphotransferase** system) phosphorylation cascade. Using immobilized combinatorial peptide libraries and phosphorimaging, heptapeptides and octapeptides were identified which selectively inhibit EI in vitro. The IC50 of the best peptides is 30 .mu.M which is close to the KM (6 .mu.M) of EI for its natural substrate HPr (histidine contg. phosphoryl carrier protein of the **PTS**). The affinity-selected peptides are better inhibitors than a peptide with the active-site sequence of HPr The selected peptides contain several basic residues and one arom. residue which do not occur in the active site of HPr. The large proportion of basic residues most likely reflects charge complementarity to the strongly acidic active-site pocket of EI. Guanidino groups might facilitate by complexation of the phosphoryl group the slow phosphorylation of the peptide.

L18 ANSWER 7 OF 24 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1998143423 MEDLINE
DOCUMENT NUMBER: 98143423 PubMed ID: 9484892
TITLE: Control of the expression of the manXYZ operon in Escherichia coli: Mlc is a negative regulator of the mannose **PTS**.

AUTHOR: Plumbridge J
CORPORATE SOURCE: Institut de Biologie Physico-chimique (UPR9073), Paris, France.. plumbridge@ibpc.fr
SOURCE: MOLECULAR MICROBIOLOGY, (1998 Jan) 27 (2) 369-80.
Journal code: MOM; 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D90825
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980410
Last Updated on STN: 19980410
Entered Medline: 19980331

AB The manXYZ operon of Escherichia coli encodes a sugar transporter of the phosphoenol **pyruvate** (**PEP**)-dependent phosphotransferase system, which is capable of transporting many sugars, including glucose, mannose and the aminosugars, glucosamine and N-acetylglucosamine. Transcription of manX is strongly dependent on cyclic AMP (cAMP)/cAMP receptor protein (CAP). A cAMP/CAP binding site is located at -40.5, and activation by cAMP/CAP is shown to be typical of a class II promoter. The 5' end of a transcript, potentially encoding two proteins, is expressed divergently from the manXYZ operon. Previously, two binding sites for the NagC repressor were detected upstream of manX, but a mutation in nagC has very little effect on manX expression. However, a mutation in the mlc gene, encoding a homologue of nagC, results in a threefold derepression of manX expression, suggesting that this protein is a more important regulator of manX expression than NagC. The Mlc protein binds to the NagC operators, binding preferentially to the promoter-proximal operator. Plasmids overproducing either the NagC protein or the Mlc protein repress the expression of manX, but the effect of the Mlc protein is stronger. The mlc gene is shown to be allelic with the previously characterized dgsA mutation affecting the mannose phosphoenolpyruvate-dependent phosphotransferase system (**PTS**).

L18 ANSWER 8 OF 24 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 96434331 MEDLINE
DOCUMENT NUMBER: 96434331 PubMed ID: 8805571
TITLE: The first step in sugar transport: crystal structure of the amino terminal domain of enzyme I of the E. coli **PEP: sugar phosphotransferase** system and a model of the phosphotransfer complex with HPr.
AUTHOR: Liao D I; Silverton E; Seok Y J; Lee B R; Peterkofsky A; Davies D R
CORPORATE SOURCE: Laboratory of Molecular Biology, NIDDK, National Institutes of Health, Bethesda, MD 20892, USA.
SOURCE: STRUCTURE, (1996 Jul 15) 4 (7) 861-72.
Journal code: B31; 9418985. ISSN: 0969-2126.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L15191; GENBANK-L46341; GENBANK-M10425; GENBANK-M81756; GENBANK-M98359; GENBANK-U12340; GENBANK-U15110; GENBANK-Z37113; SWISSPROT-P12654; SWISSPROT-P23388; SWISSPROT-P23533; SWISSPROT-P23536
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970507
Last Updated on STN: 19970507
Entered Medline: 19970430

AB BACKGROUND: The bacterial phosphoenolpyruvate (**PEP**): **sugar phosphotransferase** system (**PTS**)

transports exogenous hexose sugars through the membrane and tightly couples transport with phosphoryl transfer from **PEP** to the sugar via several phosphoprotein intermediates. The phosphate group is first transferred to enzyme I, second to the histidine-containing phosphocarrier protein HPr, and then to one of a number of sugar-specific enzymes II. The structures of several HPrs and enzymes IIA are known. Here we report the structure of the N-terminal half of enzyme I from Escherichia coli (EIN). RESULTS: The crystal structure of EIN (MW approximately 30 kDa) has been determined and refined at 2.5 A resolution. It has two distinct structural subdomains; one contains four alpha helices arranged as two hairpins in a claw-like conformation. The other consists of a beta sandwich containing a three-stranded antiparallel beta sheet and a four-stranded parallel beta sheet, together with three short alpha helices. Plausible models of complexes between EIN and HPr can be made without assuming major structural changes in either protein. CONCLUSIONS: The alpha/beta subdomain of EIN is topologically similar to the phosphohistidine domain of the enzyme **pyruvate** phosphate dikinase, which is phosphorylated by **PEP** on a histidyl residue but does not interact with HPr. It is therefore likely that features of this subdomain are important in the autophosphorylation of enzyme I. The helical subdomain of EIN is not found in **pyruvate** phosphate dikinase; this subdomain is therefore more likely to be involved in phosphoryl transfer to HPr.

L18 ANSWER 9 OF 24 MEDLINE
ACCESSION NUMBER: 97141345 MEDLINE
DOCUMENT NUMBER: 97141345 PubMed ID: 8987689
TITLE: A direct comparison of approaches for increasing carbon flow to aromatic biosynthesis in Escherichia coli.
AUTHOR: Gosset G; Yong-Xiao J; Berry A
CORPORATE SOURCE: Instituto de Biotecnologia, Universidad Nacional Autonoma de Mexico, Cuernavaca, Morelos, Mexico.
SOURCE: JOURNAL OF INDUSTRIAL MICROBIOLOGY, (1996 Jul) 17 (1) 47-52.
Journal code: ALF; 8610887. ISSN: 0169-4146.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: B
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19970219
Entered Medline: 19970130

AB Different approaches to increasing carbon commitment to aromatic amino acid biosynthesis were compared in isogenic strains of Escherichia coli. In a strain having a wild-type **PEP**:glucose phosphotransferase (**PTS**) system, inactivation of the genes encoding **pyruvate** kinase (pykA and pykF) resulted in a 3.4 fold increase in carbon flow to aromatic biosynthesis. In a strain already having increased carbon flow to aromatics by virtue of overexpression of the tktA gene (encoding transketolase), the pykA and/or pykf mutations had no effect. A **PTS**- glucose+ mutant showed a 1.6-fold increase in carbon flow to aromatics compared to the **PTS**+ control strain. In the **PTS**- glucose+ host background, overexpression of tktA caused a further 3.7-fold increase in carbon flow, while inactivation of pykA and pykF caused a 5.8-fold increase. When all of the variables tested (**PTS**-glucose+, pykA, pykF, and overexpressed tktA) were combined in a single strain, a 19.9-fold increase in carbon commitment to aromatic biosynthesis was achieved.

L18 ANSWER 10 OF 24 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 96:70638 SCISEARCH

THE GENUINE ARTICLE: TP313
TITLE: CURRENT RESEARCH ON THE GENETICS OF LACTIC-ACID PRODUCTION IN LACTIC-ACID BACTERIA
AUTHOR: DAVIDSON B E (Reprint); LLANOS R M; CANCILLA M R; REDMAN N C; HILLIER A J
CORPORATE SOURCE: UNIV MELBOURNE, DEPT BIOCHEM, PARKVILLE, VIC 3052, AUSTRALIA (Reprint); CSIRO, DIV FOOD SCI & TECHNOL, DAIRY RES LAB, HIGHETT, VIC 3190, AUSTRALIA
COUNTRY OF AUTHOR: AUSTRALIA
SOURCE: INTERNATIONAL DAIRY JOURNAL, (1995) Vol. 5, No. 8, pp. 763-784.
ISSN: 0958-6946.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: AGRI
LANGUAGE: ENGLISH
REFERENCE COUNT: 101
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Lactic acid derived from lactose is a major by-product of energy production in lactic acid bacteria. The uptake of lactose by these organisms is mediated either by the lactose phosphoenolpyruvate-phosphotransferase system (lactose **PEP-PTS**), or by a lactose-proton symport system. The disaccharide is then converted to lactate with the concomitant production of ATP. In Lactococcus lactis the genes encoding the lactose **PEP-PTS**, phospho-beta-galactosidase and the tagatose 6-phosphate pathway enzymes are plasmid encoded, while other genes required for lactate synthesis, including those of the Embden-Meyerhof pathway, are on the chromosome. We have compiled a current list of genes required for lactate synthesis in the lactic acid bacteria that have been cloned and characterized and discuss the present status of genetic research in this area. The analyses of the L. lactic lac operon have yielded one of the most detailed pictures of genetic regulation in the bacterium. The operon has been fully sequenced, the regulatory protein LacR which represses lac operon transcription has been purified and its properties determined, and the operon promoters and operators have been identified. Investigations of chromosomally encoded L. lactis genes have resulted in the identification and characterization of pfk, pyk, idh, tpi, and gap, which encode phosphofructokinase, **pyruvate** kinase, L-(+)-lactate dehydrogenase, triosephosphate isomerase and glyceraldehyde-3-phosphate dehydrogenase, respectively. All of these enzymes (except triosephosphate isomerase) are known from previous studies to be important in metabolite level regulation of the pathway. pfk, pyk and idh are organized into a tricistronic operon (the las operon), while tpi and gap are in monocistronic units. The las operon is so far unique to L. lactis. A number of investigators have studied the effect of gene dosage on glycolytic flux in lactic acid bacteria and their results are reviewed. We have introduced multiple copies of pfk, pyk, idh and the las operon into L. lactis and report the effect of the increase in gene dosage on enzyme levels and the rate of lactic acid production.

L18 ANSWER 11 OF 24 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 95093612 MEDLINE
DOCUMENT NUMBER: 95093612 PubMed ID: 8000534
TITLE: Vesicles prepared from Streptococcus mutans demonstrate the presence of a second glucose transport system.
AUTHOR: Buckley N D; Hamilton I R
CORPORATE SOURCE: Department of Oral Biology, Faculty of Dentistry, University of Manitoba, Winnipeg, Canada.
SOURCE: MICROBIOLOGY, (1994 Oct) 140 (Pt 10) 2639-48.
Journal code: BXW; 9430468. ISSN: 1350-0872.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199501
ENTRY DATE: Entered STN: 19950215
Last Updated on STN: 19950215
Entered Medline: 19950120

AB Streptococcus mutans, an important aetiological agent of dental caries, is known to transport glucose via the phosphoenolpyruvate (**PEP**) phosphotransferase system (**PTS**). An alternative non-**PTS** glucose transport system in S. mutans Ingbritt was suggested by the increased ATP-dependent phosphorylation of glucose and the presence of higher cellular concentrations of free glucose in cells grown in continuous culture under **PTS**-repressed conditions compared to those resulting in optimal **PTS** activity. A method was developed for the preparation of membrane vesicles in order to study this system in the absence of **PTS** activity. These vesicles had very low activity of the cytoplasmic enzymes, glucokinase, **pyruvate** kinase and lactate dehydrogenase. This, coupled with the lack of glycolytic activity and the inability to transport glucose, suggested that the vesicles would also be deficient in **PTS** activity because of the absence of the general soluble **PTS** proteins, Enzyme I and HPr, required for the transport of all **PTS** sugars. Freeze-fracture electron microscopy and membrane H(+)-ATPase analysis indicated that over 90% of the vesicles had a right-side-out orientation. Vesicles from cells grown in continuous culture under **PTS** -dominant and **PTS**-repressed conditions both exhibited glucose counterflow. This indicates the presence of a constitutive non-**PTS** carrier in the organism capable of transporting glucose and utilizing ATP for glucose phosphorylation. Analysis of growth yields of cells grown under **PTS**-repressed and **PTS**-optimal conditions suggests that ATP, or an equivalent high energy molecule, must be involved in the actual transport process. This analysis is consistent with an ATP-binding protein model such as the Msm transport system reported by R. R. B. Russell and coworkers (J Biol Chem 267, 4631-4637), but it does not exclude the possibility of a separate permease for glucose.

L18 ANSWER 12 OF 24 MEDLINE
ACCESSION NUMBER: 93393384 MEDLINE
DOCUMENT NUMBER: 93393384 PubMed ID: 8216508
TITLE: Transport and metabolism of glucose and arabinose in Bifidobacterium breve.
AUTHOR: Degnan B A; Macfarlane G T
CORPORATE SOURCE: Medical Research Council, Dunn Clinical Nutrition Centre, Cambridge, UK.
SOURCE: ARCHIVES OF MICROBIOLOGY, (1993) 160 (2) 144-51.
Journal code: 7YN; 0410427. ISSN: 0302-8933.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199310
ENTRY DATE: Entered STN: 19931105
Last Updated on STN: 19931105
Entered Medline: 19931021

AB Glucose was required for the transport of arabinose into Bifidobacterium breve. The non-metabolisable glucose analogue 2-deoxy-D-glucose (2-DG) did not facilitate assimilation of arabinose. Studies using D-[U-14C]-labelled arabinose showed that it was fermented to **pyruvate**, formate, lactate and acetate, whereas the principal metabolic products of D-[U-14C]-labelled glucose were acetate and formate. In contrast to glucose, arabinose was not incorporated into cellular macromolecules. A variety of metabolic inhibitors and inhibitors of sugar transport (proton

ionophores, metal ionophores, compounds associated with electron transport) were used to investigate the mechanisms of sugar uptake. Only NaF, an inhibitor of substrate level phosphorylation, and 2-DG inhibited glucose assimilation. 2-DC had no effect on arabinose uptake, but NaF was stimulatory. High levels of phosphorylation of glucose and 2-DC by **PEP** and to a lesser degree, ATP were seen in phosphoenolpyruvate: phosphotransferase (**PEP**:**PTS**) assays. These data together with strong inhibition of glucose uptake by NaF suggest a role for phosphorylation in the transport process. Arabinose uptake in B. breve was not directly dependent on phosphorylation or any other energy-linked form of transport but may be assimilated by glucose-dependent facilitated diffusion.

L18 ANSWER 13 OF 24 MEDLINE
ACCESSION NUMBER: 92269758 MEDLINE
DOCUMENT NUMBER: 92269758 PubMed ID: 1534139
TITLE: A novel mutation FruS, altering synthesis of components of the phosphoenolpyruvate: fructose phosphotransferase system in Escherichia coli K12.
AUTHOR: Bolshakova T N; Molchanova M L; Erlagaeva R S; Grigorenko Y A; Gershanovitch V N
CORPORATE SOURCE: N.F. Gamaleya Institute for Epidemiology and Microbiology, Academy of Medical Sciences, Moscow, USSR.
SOURCE: MOLECULAR AND GENERAL GENETICS, (1992 Apr) 232 (3) 394-8. Journal code: NGP; 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199206
ENTRY DATE: Entered STN: 19920710
Last Updated on STN: 19920710
Entered Medline: 19920619

AB A novel mutation, FruS localised in the fru operon was obtained. It uncouples expression of the genes determining synthesis of the fructose-specific transport proteins and fructose-1-phosphate kinase. In FruS bacteria the fruA and fruF genes (coding for Enzyme IIfru and FPr, respectively) are constitutive by expressed while fruK (encoding fructose-1-phosphate kinase) remains inducible. In contrast to other mutations, which render expression of the whole fru operon constitutive, the FruS mutation: (1) does not lead to D-xylitol sensitivity; (2) does not inhibit growth on D-lactate, **pyruvate** and L-alanine; (3) does not decrease phosphoenolpyruvate (**PEP**) synthase activity.

L18 ANSWER 14 OF 24 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 93051364 MEDLINE
DOCUMENT NUMBER: 93051364 PubMed ID: 1427100
TITLE: Cloning, sequencing and expression in Escherichia coli of the ptsI gene encoding enzyme I of the phosphoenolpyruvate: **sugar phosphotransferase** transport system from Streptococcus salivarius.
AUTHOR: Gagnon G; Vadeboncoeur C; Levesque R C; Frenette M
CORPORATE SOURCE: Departement de Biochimie (Sciences), Universite Laval, Ste-Foy, Quebec, Canada.
SOURCE: GENE, (1992 Nov 2) 121 (1) 71-8. Journal code: FOP; 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M79310; GENBANK-M81114; GENBANK-M81115; GENBANK-M81116; GENBANK-M81117; GENBANK-M81118;

GENBANK-M81756; GENBANK-M95864; GENBANK-X65112; GENBANK-X65113
ENTRY MONTH: 199212
ENTRY DATE: Entered STN: 19930122
Last Updated on STN: 19930122
Entered Medline: 19921211

AB We present the cloning and sequencing of the ptsI gene, encoding enzyme I (EI) of the phosphoenolpyruvate (**PEP**): **sugar phosphotransferase** (**PTS**) transport system from Streptococcus salivarius. The ptsI gene corresponds to an open reading frame of 1731 nucleotides, which translates into a putative 577-amino acid (aa) protein with a M(r) of 62,948 and a pI of 4.49. The EI was produced in Escherichia coli under the control of its own promoter located immediately upstream of ptsI, a situation never previously reported for any other gene coding for an EI. The deduced aa sequence of the S. salivarius EI shows a high degree of similarity with the E. coli EI and the EI moiety of the multiphosphoryl transfer protein from Rhodobacter capsulatus. The S. salivarius EI also shares a highly conserved aa cluster with a non-**PTS** protein, the maize **pyruvate** :orthophosphate dikinase. The conserved cluster is located in a domain which is hypothesized to be the **PEP**-binding site.

L18 ANSWER 15 OF 24 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1990:625291 HCAPLUS
DOCUMENT NUMBER: 113:225291
TITLE: On the evolutionary origins of the bacterial phosphoenolpyruvate:**sugar phosphotransferase** system
AUTHOR(S): Wu, L. F.; Saier, M. H., Jr.
CORPORATE SOURCE: Dep. Biol., C-016, Univ. California, San Diego, La Jolla, CA, 92093, USA
SOURCE: Mol. Microbiol. (1990), 4(7), 1219-22
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The genes encoding the proteins of the fructose-specific phosphotransferase system (**PTS**) of Rhodobacter capsulatus were sequenced, and the deduced amino acyl sequences of the energy-coupling protein, Enzyme I, and the transport protein, Enzyme IIfru, were compared with published sequences. Enzyme I was found to be homologous to **pyruvate**:phosphate dikinase of plants, while Enzyme IIfru was found to be homologous to the insulin-responsive glucose facilitator of mammals. The evolutionary and functional implications of these findings are discussed.

L18 ANSWER 16 OF 24 MEDLINE
ACCESSION NUMBER: 89384462 MEDLINE
DOCUMENT NUMBER: 89384462 PubMed ID: 2674659
TITLE: The repressor of the **PEP**:fructose phosphotransferase system is required for the transcription of the pps gene of Escherichia coli.
AUTHOR: Geerse R H; van der Pluijm J; Postma P W
CORPORATE SOURCE: E.C. Slater Institute for Biochemical Research, University of Amsterdam, The Netherlands.
SOURCE: MOLECULAR AND GENERAL GENETICS, (1989 Aug) 218 (2) 348-52.
Journal code: NGP; 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198910
ENTRY DATE: Entered STN: 19900309

Last Updated on STN: 19900309
Entered Medline: 19891016

AB We have cloned the pps gene, coding for **PEP** synthase, of Escherichia coli. **PEP** synthase catalyses the ATP-dependent conversion of **pyruvate** into phosphoenol-**pyruvate** and is required for gluconeogenesis. The pps gene was cloned by an in vivo cloning method using a mini-Mulac bacteriophage containing a plasmid replicon. Upon expression of the cloned pps gene in the maxicell system a protein with an apparent molecular weight of 84 kDa was synthesized. The position of the pps gene of the plasmid was localized by restriction analysis of isolated transposon insertions and the determination of the **PEP** synthase activities of the different clones. An operon fusion between the pps gene and the galK gene was constructed. Measurements of the galactokinase activity in Salmonella typhimurium galK and galK fruR mutants showed that the transcription of the pps gene requires the presence of FruR, the repressor of the **PEP**: fructose phosphotransferase system (**PTS**) in E. coli and S. typhimurium. To test whether the components of the Fructose **PTS**, in particular FPr, are involved in the expression of the pps gene, we investigated a S. typhimurium galK strain, containing the fusion plasmid, in which the chromosomal fru operon was inactivated by a transposon insertion. Measurements of the galactokinase activity showed that the absence of the Fructose **PTS** proteins has no significant influence on the regulation of the pps gene.

L18 ANSWER 17 OF 24 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 87:51976 LIFESCI
TITLE: Phosphoenol-**pyruvate:sugar phosphotransferase** systems and sugar metabolism in Brevibacterium flavum .
AUTHOR: Mori, M.; Shiio, I.
CORPORATE SOURCE: Cent. Res. Lab., Ajinomoto Co., Ltd., Kawasaki-ku, Kawasaki, Kanagawa 210, Japan
SOURCE: AGRIC. BIOL. CHEM., (1987) vol. 51, no. 10, pp. 2671-2678.
DOCUMENT TYPE: Journal
FILE SEGMENT: J
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Brevibacterium flavum mutants defective in the phosphoenolpyruvate (**PEP**)-dependent glucose phosphotransferase system (**PTS**) were selected with high frequency by 2-deoxyglucose-resistance. Most of them (DOG super(r)) still had the fructose-**PTS** and grew not only on fructose but also on glucose like the wild-type strain. A mutant having 1/8th the fructose-**PTS** activity of the wild strain but normal glucose-**PTS** activity was isolated as a xylitol-resistant mutant. It grew on glucose but not on fructose. The glucose-**PTS** was active on glucose, glucosamine, 2-deoxyglucose and mannose, and slightly on methyl- alpha -glucoside and N-acetylglucosamine, but not on fructose or xylitol. The fructose-**PTS** acted on fructose and xylitol, and to some extent on glucose but not on glucosamine or 2-deoxyglucose. Mutants unable to grow on glucose (DOG super(r)Glc super(-)) derived from a DOG super(r) mutant were all defective in the fructose-**PTS**.

L18 ANSWER 18 OF 24 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 7
ACCESSION NUMBER: 1987:277727 BIOSIS
DOCUMENT NUMBER: BA84:18766
TITLE: **PYRUVATE** FORMATION AND SUGAR METABOLISM IN AN AMINO ACID-PRODUCING BACTERIUM BREVIBACTERIUM-FLAVUM.
AUTHOR(S): MORI M; SHIIO I
CORPORATE SOURCE: CENT. RES. LAB., AJINOMOTO CO. INC., KAWASAKI-KU, KAWASAKI, KANAGAWA 210, JPN.

SOURCE: AGRIC BIOL CHEM, (1987) 51 (1), 129-138.
CODEN: ABCHA6. ISSN: 0002-1369.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB A Brevibacterium flavum mutant lacking **pyruvate** kinase, No. 70, grew on glucose, fructose and sucrose as well as the original wild strain did, but was unable to grow on ribose or gluconate unless **pyruvate** was added. Mutants that required **pyruvate** for growth on ribose were derived directly from the wild strain. Many of them were completely or partially defective in **pyruvate** kinase activity. These **pyruvate** kinase mutants were also unable to grow on gluconate. A phosphoenolpyruvate (**PEP**): **sugar phosphotransferase** system (**PTS**) was found in B. flavum, which catalyzed the formation of **pyruvate** and sugar phosphate from **PEP** and sugar. The system required Mg2+, acted on glucose, fructose, mannose, glucosamine and 2-deoxyglucose, and existed in the cells grown on any of the carbon sources tested. Cells grown on fructose, mannitol and sucrose, however, exhibited higher **PTS** activities on fructose than those grown on others. Glucose **PTS** activity was about 20-fold stronger than that of glucokinase. Other sugar metabolic enzymes, inducible mannitol dehydrogenase, gluconokinase, ribokinase and maltase, as well as constitutive invertase were also detected. Oxaloacetate decarboxylase and malic enzyme, which also catalyzed the **pyruvate** formation, were found in B. flavum, but the latter activity was very low in cells grown on glucose. The levels of these enzymes in **pyruvate** kinase mutants unable to grow on ribose or gluconate derived from the wild strain were almost identical to those in the wild-type strain.

L18 ANSWER 19 OF 24 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1986:64690 HCAPLUS
DOCUMENT NUMBER: 104:64690
TITLE: Reconstitution of regulatory properties of adenylate cyclase in Escherichia coli extracts
AUTHOR(S): Reddy, Prasad; Meadow, Norman; Roseman, Saul; Peterkofsky, Alan
CORPORATE SOURCE: Lab. Biochem. Genet., Natl. Heart, Lung Blood Inst., Bethesda, MD, 20892, USA
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1985), 82(24), 8300-4
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The inhibition of adenylate cyclase (I) activity of E. coli by Me .alpha.-glucoside was demonstrated in intact or in permeable cells, but not in cell-free exts. In intact or permeable cells, this inhibition was demonstrable only in strains expressing the genes for proteins of the phosphoenolpyruvate-**sugar phosphotransferase** system (**PTS**); in permeable cells, the inhibition also requires K2HPO4. By using homogeneous proteins of the **PTS**, it was possible to reconstitute in cell-free exts. many of the features of the regulated form of adenylate cyclase. In the absence of K2HPO4, permeable cells had lower I activity than exts.; addn. of homogeneous **PTS** proteins to the exts. brought I activity close to the level obsd. in permeable cells. The low activity obsd. in permeable cells was stimulated by K2HPO4; this stimulation was also obsd. in exts. supplemented with **PTS** proteins and **PEP**. In permeable cells, K2HPO4-stimulated I activity was inhibited by Me .alpha.-glucoside or **pyruvate**; exts. behaved similarly when supplemented with **PTS** proteins, K2HPO4, and **PEP**. Thus, the regulated form of adenylate cyclase was reconstituted in cell-free exts. by addn. of homogeneous **PTS** proteins.

L18 ANSWER 20 OF 24 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 85:56777 LIFESCI
TITLE: Phosphorylation of hexoses in Streptomyces aureofacines : Evidence that the phosphoenol-**pyruvate**: **sugar phosphotransferase** system is not operative.
AUTHOR: Novotna, J.; Hostalek, Z.
CORPORATE SOURCE: Inst. Microbiol., Czechoslovak Acad. Sci., 142 20 Prague 4, Czechoslovakia
SOURCE: FEMS MICROBIOL. LETT., (1985) vol. 28, no. 3, pp. 347-350.
DOCUMENT TYPE: Journal
FILE SEGMENT: J; A
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Sugar phosphates are formed in cell-free extracts of Streptomyces aureofacines RIA57 from glucose of fructose in the presence of phosphoenolpyruvate. In contrast to the phosphorylation by adenosine 5'-triphosphate the kinetics of formation of glucose 6-phosphate via phosphoenolpyruvate (**PEP**) is nonlinear. The product of fructose phosphorylation (only fructose 6-phosphate was determined by paper chromatography) and the absence of 1-phosphofructokinase indicate that fructose metabolism in S. aureofaciens does not proceed via the phosphoenolpyruvate:**sugar phosphotransferase** system (**PTS**).

L18 ANSWER 21 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 78366270 EMBASE
DOCUMENT NUMBER: 1978366270
TITLE: The mechanism of sugar-dependent repression of synthesis of catabolic enzymes in Escherichia coli.
AUTHOR: Gonzalez J.E.; Peterkofsky A.
CORPORATE SOURCE: Lab. Biochem. Genet., Nat. Heart Lung Blood Inst., NIH, Bethesda, Md. 20014, United States
SOURCE: Progress in Clinical and Biological Research, (1978) VOL.22/- (325-332).
CODEN: PCBRD2
COUNTRY: United States
DOCUMENT TYPE: Journal
FILE SEGMENT: 004 Microbiology
029 Clinical Biochemistry
LANGUAGE: English
AB Previous studies have indicated that the E. coli adenylate cyclase (AC) activity is controlled by an interaction with the phosphoenolpyruvate (**PEP**) : **sugar phosphotransferase** system (**PTS**). A model for the regulation of AC involving the phosphorylation state of the **PTS** is described. Kinetic studies support the concept that the velocity of AC is determined by the opposing contributions of **PEP**-dependent phosphorylation (V1) and sugar-dependent dephosphorylation (V2) of the **PTS** proteins according to the expression % V(AC) = 100 /[1 + (Max V2/Max V1)]. Physiological parameters influencing the rate of the **PTS** are discussed in the framework of their effects on cAMP metabolism. Factors that increase cellular concentration of **PEP** (and stimulate V1) appear to enhance AC activity while increases in extracellular sugar concentration (which stimulate V2) or internal levels of **pyruvate** (which inhibit V1) inhibit the activity of this enzyme.

L18 ANSWER 22 OF 24 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 79155259 MEDLINE
DOCUMENT NUMBER: 79155259 PubMed ID: 219294
TITLE: The Escherichia coli adenylate cyclase complex: activation by phosphoenolpyruvate.

AUTHOR: Peterkofsky A; Gazdar C
SOURCE: JOURNAL OF SUPRAMOLECULAR STRUCTURE, (1978) 9 (2) 219-30.
Journal code: K75; 0330464. ISSN: 0091-7419.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197906
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 19980206
Entered Medline: 19790629

AB A model for the regulation of the activity of Escherichia coli adenylate cyclase is presented. It is proposed that Enzyme I of the phosphoenolpyruvate:**sugar phosphotransferase** system (**PTS**) interacts in a regulatory sense with the catalytic unit of adenylate cyclase. The phosphoenolpyruvate (**PEP**)-dependent phosphorylation of Enzyme I is assumed to be associated with a high activity state of adenylate cyclase. The **pyruvate** or sugar-dependent dephosphorylation of Enzyme I is correlated with a low activity state of adenylate cyclase. Evidence in support of the proposed model involves the observation that Enzyme I mutants have low cAMP levels and that **PEP** increases cellular cAMP levels and, under certain conditions, activates adenylate cyclase, Kinetic studies indicate that various ligands have opposing effects on adenylate cyclase. While **PEP** activates the enzyme, either glucose or **pyruvate** inhibit it. The unique relationships of **PEP** and Enzyme I to adenylate cyclase activity are discussed.

L18 ANSWER 23 OF 24 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 78070166 MEDLINE
DOCUMENT NUMBER: 78070166 PubMed ID: 338995
TITLE: The mechanism of sugar-dependent repression of synthesis of catabolic enzymes in Escherichia coli.
AUTHOR: Gonzalez J E; Peterkofsky A
SOURCE: JOURNAL OF SUPRAMOLECULAR STRUCTURE, (1977) 6 (4) 495-502.
Journal code: K75; 0330464. ISSN: 0091-7419.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197802
ENTRY DATE: Entered STN: 19900314
Last Updated on STN: 19980206
Entered Medline: 19780218

AB Previous studies have indicated that the Escherichia coli adenylate cyclase (AC) activity is controlled by an interaction with the phosphoenolpyruvate (**PEP**): **sugar phosphotransferase** system (**PTS**). A model for the regulation of AC involving the phosphorylation state of the **PTS** is described. Kinectic studies support the concept that the velocity of AC is determined by the opposing contributions of **PEP**-dependent phosphorylation (V1) and sugar-dependent dephosphorylation (V2) of the **PTS** proteins according to the expression percent VAC=100/[1 + (Max V2/Max V1)]. Physiological parameters influencing the rate of the **PTS** are discussed in the framework of their effects on cAMP metabolism. Factors that increase cellular concentration of **PEP** (and stimulate V1) appear to enhance AC activity while increases in extracellular sugar concentration (which stimulate V2) or internal levels of **pyruvate** (which inhibit V1) inhibit the activity of this enzyme.

L18 ANSWER 24 OF 24 EMBASE

ACCESSION NUMBER: 77193220 EMBASE
DOCUMENT NUMBER: 1977193220
TITLE: Regulation of lactose fermentation in group N streptococci.
AUTHOR: Thomas T.D.
CORPORATE SOURCE: New Zealand Dairy Res. Inst., Palmerston North, New Zealand
SOURCE: Applied and Environmental Microbiology, (1976) 32/4 (474-478).
CODEN: AEMIDF
DOCUMENT TYPE: Journal
FILE SEGMENT: 004 Microbiology
LANGUAGE: English

AB Group N streptococci, which have the lactose phosphoenolpyruvate (**PEP**) dependent phosphotransferase system (**PTS**) and phospho .beta. D galactosidase (.beta. Pgal), grew rapidly on lactose and converted more than 90% of the sugar to L lactate. In contrast, Streptococcus lactis 7962, which does not have a .beta. Pgal, grew slowly on lactose and converted only 15% of the sugar to L lactate. With glucose and galactose, this strain had growth rates and fermentation patterns similar to those of other S. lactis strains, suggesting that the rapid and homolactic fermentation of lactose that is characteristic of group N streptococci is dependent upon a functional **PEP** dependent **PTS** and the presence of .beta. Pgal. Seventeen strains of group N streptococci were examined for the activator specificities of **pyruvate** kinase and lactate dehydrogenase. The properties of each enzyme from all the strains, including S. lactis 7962, were similar. **Pyruvate** kinase had a broad activator specificity, whereas activation of lactate dehydrogenase was specific for ketohexose diphosphate. All intermediates of lactose metabolism from the hexose phosphates to the triose phosphates activated **pyruvate** kinase. No activation was obtained with adenosine 5' monophosphate. K+ and Mg2+ were required for **pyruvate** kinase activity but could be replaced by NH4+ and Mn2+, respectively. Lactate dehydrogenase was activated equally by fructose 1,6 diphosphate and tagatose 1,6 diphosphate, the activation characteristics being pH dependent. The roles of **pyruvate** kinase and lactate dehydrogenase in the regulation of lactose fermentation by group N streptococci are discussed.

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(FILE 'HOME' ENTERED AT 13:57:34 ON 01 APR 2002)

FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS, LIFESCI' ENTERED AT 13:57:58 ON 01 APR 2002

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L1          5706 S CORYNEBACTERIUM (A)GLUTAMICUM
L2             0 S PHOSPHOENYLPYRUVATE (W)SUGAR (W)PHOSPHOTRANSFERASE?
L3          3480 S "SUGAR PHOSPHOTRANSFERASE?"
L4            11 S PHOSPHOENYLPYRUVATE
L5            16 S L1 AND L3
L6            10 DUP REM L5 (6 DUPLICATES REMOVED)
L7         19911 S "PTS"
L8          1406 S L3 AND L7
L9        152465 S PYRUVATE
L10          146 S L8 AND L9
L11            0 S L1 AND L10
L12        11661 S BREVIBACTERIUM
L13            5 S L12 AND L10
L14            2 DUP REM L13 (3 DUPLICATES REMOVED)
L15          473 S L3 AND "PEP"
L16          280 S L15 AND L7
L17           48 S L9 AND L16
L18           24 DUP REM L17 (24 DUPLICATES REMOVED)
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=> s l18 and l1
L19           0 L18 AND L1

=> e pompejus m/au
E1            3      POMPEIUS P/AU
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E4           22      POMPEJUS MARKUS/AU
E5           37      POMPEKIRN V/AU
E6            1      POMPEL M/AU
E7            1      POMPEL P/AU
E8            1      POMPELEAN A/AU
E9            1      POMPELIA D MICK/AU
E10           2      POMPELIA DONALD M/AU
E11           2      POMPELIANO O/AU
E12         214      POMPELLA A/AU

=> s e3
L20          26 "POMPEJUS M"/AU

=> s e3-e4
L21          48 ("POMPEJUS M"/AU OR "POMPEJUS MARKUS"/AU)

=> e kroger b/au
E1            2      KROGER ANDREW/AU
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E3           92 --> KROGER B/AU
E4            6      KROGER B J/AU
E5            1      KROGER BERND/AU
E6            1      KROGER BERNHARD/AU
E7            4      KROGER BLOCK A/AU
E8           15      KROGER BURKHARD/AU
E9           75      KROGER C/AU
E10          21      KROGER C F/AU
E11           1      KROGER C R/AU
E12           1      KROGER C S/AU

=> s e3
L22          92 "KROGER B"/AU

=> e schroder h/au
E1            1      SCHRODER GUSTAV ADOLF/AU
E2            1      SCHRODER GUY/AU
E3         1910 --> SCHRODER H/AU
E4           45      SCHRODER H A/AU
E5          727      SCHRODER H C/AU
E6            5      SCHRODER H CH/AU
E7            1      SCHRODER H CORRECTED TO SCHODER H/AU
E8          365      SCHRODER H D/AU
E9            1      SCHRODER H D A A/AU
E10           1      SCHRODER H DAA/AU
E11          98      SCHRODER H E/AU
E12          60      SCHRODER H F/AU

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L23        1910 "SCHRODER H"/AU

=> e zelder o/au
E1            3      ZELDER J/AU
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E3          180 --> ZELDER O/AU
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E9            1      ZELDERS H G/AU
E10           2      ZELDERS I T/AU
E11          16      ZELDERS T/AU
E12           1      ZELDERS THEO/AU

=> s e3
L24         180 "ZELDER O"/AU

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E2            1      HABERHAUER F/AU
E3          197 --> HABERHAUER G/AU
E4           12      HABERHAUER GEBHARD/AU
E5           20      HABERHAUER GEORG/AU
E6            7      HABERHAUER GREGOR/AU
E7            2      HABERHAUER GUENTHER/AU
E8            1      HABERHAUER HELMUT/AU
E9            5      HABERHAUER HELMUTH/AU
E10           1      HABERHAUER OSWALD/AU
E11          12      HABERHAUER P/AU
E12           2      HABERHAUER PETER/AU

=> s e3-e6
L25         236 ("HABERHAUER G"/AU OR "HABERHAUER GEBHARD"/AU OR "HABERHAUER
                GEORG"/AU OR "HABERHAUER GREGOR"/AU)

=> d his

     (FILE 'HOME' ENTERED AT 13:57:34 ON 01 APR 2002)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 13:57:58 ON 01 APR 2002
L1          5706 S CORYNEBACTERIUM (A)GLUTAMICUM
L2             0 S PHOSPHOENYLPYRUVATE (W)SUGAR (W)PHOSPHOTRANSFERASE?
L3          3480 S "SUGAR PHOSPHOTRANSFERASE?"
L4            11 S PHOSPHOENYLPYRUVATE
L5            16 S L1 AND L3
L6            10 DUP REM L5 (6 DUPLICATES REMOVED)
L7         19911 S "PTS"
L8          1406 S L3 AND L7
L9        152465 S PYRUVATE
L10          146 S L8 AND L9
L11            0 S L1 AND L10
L12        11661 S BREVIBACTERIUM
L13            5 S L12 AND L10
L14            2 DUP REM L13 (3 DUPLICATES REMOVED)
L15          473 S L3 AND "PEP"
L16          280 S L15 AND L7
L17           48 S L9 AND L16
L18           24 DUP REM L17 (24 DUPLICATES REMOVED)
L19            0 S L18 AND L1
                 E POMPEJUS M/AU
L20           26 S E3
L21           48 S E3-E4
                 E KROGER B/AU
L22           92 S E3
                 E SCHRODER H/AU
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L23        1910 S E3
                E ZELDER O/AU
L24         180 S E3
                E HABERHAUER G/AU
L25         236 S E3-E6

=> s l21 -l25
MISSING OPERATOR L21 -L25
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l21 or l22 or l23 or l24 or l25
L26       2444 L21 OR L22 OR L23 OR L24 OR L25

=> d his

     (FILE 'HOME' ENTERED AT 13:57:34 ON 01 APR 2002)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 13:57:58 ON 01 APR 2002
L1         5706 S CORYNEBACTERIUM (A)GLUTAMICUM
L2            0 S PHOSPHOENYLPYRUVATE (W)SUGAR (W)PHOSPHOTRANSFERASE?
L3         3480 S "SUGAR PHOSPHOTRANSFERASE?"
L4           11 S PHOSPHOENYLPYRUVATE
L5           16 S L1 AND L3
L6           10 DUP REM L5 (6 DUPLICATES REMOVED)
L7        19911 S "PTS"
L8         1406 S L3 AND L7
L9       152465 S PYRUVATE
L10         146 S L8 AND L9
L11           0 S L1 AND L10
L12       11661 S BREVIBACTERIUM
L13           5 S L12 AND L10
L14           2 DUP REM L13 (3 DUPLICATES REMOVED)
L15         473 S L3 AND "PEP"
L16         280 S L15 AND L7
L17          48 S L9 AND L16
L18          24 DUP REM L17 (24 DUPLICATES REMOVED)
L19           0 S L18 AND L1
                E POMPEJUS M/AU
L20          26 S E3
L21          48 S E3-E4
                E KROGER B/AU
L22          92 S E3
                E SCHRODER H/AU
L23        1910 S E3
                E ZELDER O/AU
L24         180 S E3
                E HABERHAUER G/AU
L25         236 S E3-E6
L26        2444 S L21 OR L22 OR L23 OR L24 OR L25

=> s l26 and l17
L27           0 L26 AND L17

=> s l26 and l3
L28           2 L26 AND L3

=> d 1-2 ibib ab

L28   ANSWER 1 OF 2  BIOTECHDS COPYRIGHT 2002 DERWENT INFO AND ISI
ACCESSION NUMBER: 2001-04894  BIOTECHDS
```

TITLE: Corynebacterium glutamicum nucleic acids encoding phosphoenolpyruvate:**sugar phosphotransferase** system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation; selectable marker

AUTHOR: **Pompejus M**; Kroeger B; Schroeder H; **Zelder O**; **Haberhauer G**

PATENT ASSIGNEE: BASF

LOCATION: Ludwigshafen, Germany.

PATENT INFO: WO 2001002583 11 Jan 2001

APPLICATION INFO: WO 2000-DE973 27 Jun 2000

PRIORITY INFO: DE 1999-1042097 3 Sep 1999; US 1999-142691 1 Jul 1999

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2001-080989 [09]

AB Isolated Corynebacterium glutamicum ATCC 13032 nucleic acids encoding phosphoenolpyruvate:**sugar-phosphotransferase** system (PTS) proteins or their fragments are claimed. A PTS nucleic acid (N1) does not consist of any of the F-designated genes defined and is selected from one of 17 disclosed nucleic acid sequences (S1) and their fragments nucleic acid which encode a protein selected from one of the 17 protein sequences (S2) disclosed; nucleic acid encoding a naturally occurring allelic variant of a protein selected from (S2). Also claimed are methods for producing the proteins; C. glutamicum PTS protein and its fragments; diagnosis of Corynebacterium diphtheriae infection; fusion proteins; antisense PTS nucleic acid; a method for screening molecules which modulate the activity of a PTS protein; and a transformed host cell. (144pp)

L28 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:31659 HCAPLUS

DOCUMENT NUMBER: 134:96287

TITLE: Corynebacterium glutamicum genes encoding phosphoenolpyruvate:**sugar phosphotransferase** system proteins

INVENTOR(S): **Pompejus, Markus**; Kroger, Burkhard; Schroder, Hartwig; Zelder, Oskar; **Haberhauer, Gregor**

PATENT ASSIGNEE(S): BASF Aktiengesellschaft, Germany

SOURCE: PCT Int. Appl., 143 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 6

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001002583	A2	20010111	WO 2000-IB973	20000627
WO 2001002583	A3	20010726		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-142691P P 19990701
US 1999-150310P P 19990823

DE 1999-19942095 A 19990903
DE 1999-19942097 A 19990903

AB Isolated nucleic acid mols., designated phosphoenolpyruvate:**sugar phosphotransferase** (PTS) nucleic acid mols., which encode novel PTS proteins from Corynebacterium glutamicum are described. The invention also provides antisense nucleic acid mols., recombinant expression vectors contg. PTS nucleic acid mols., and host cells into which the expression vectors have been introduced. The invention still further provides isolated PTS proteins, mutated PTS proteins, fusion proteins, antigenic peptides and methods for the improvement of prodn. of a desired compd. from C. glutamicum based on genetic engineering of PTS genes in this organism.

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L6	10	DUP REM	L5 (6 DUPLICATES REMOVED)
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L9	152465	S	PYRUVATE
L10	146	S	L8 AND L9
L11	0	S	L1 AND L10
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L18	24	DUP REM	L17 (24 DUPLICATES REMOVED)
L19	0	S	L18 AND L1
		E	POMPEJUS M/AU
L20	26	S	E3
L21	48	S	E3-E4
		E	KROGER B/AU
L22	92	S	E3

	Document ID	Issue Date	Pages	Title
1	US 20020032323 A1	20020314	64	STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES
2	US 6245502 B1	20010612	23	Target system
3	US 6162627 A	20001219	117	Methods of identifying inhibitors of sensor histidine kinases through rational drug design
4	US 6077682 A	20000620	126	Methods of identifying inhibitors of sensor histidine kinases through rational drug design

	Document ID	Issue Date	Pages	Title
1	US 6162627 A	20001219	117	Methods of identifying inhibitors of sensor histidine kinases through rational drug design
2	US 6077682 A	20000620	126	Methods of identifying inhibitors of sensor histidine kinases through rational drug design

	U	1	Document ID	Issue Date	Pages
1	☐	☐	US 20020032323 A1	20020314	64

	Title	Current OR	Current XRef
1	STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES	536/23.7	435/252.3; 435/320.1; 435/69.1; 536/24.32

	Retrieval Classif	Inventor	S	C	P	2	3	4	5
1		KUNSCH, CHARLES A. et al.	☒	☐	☐	☐	☐	☐	☐

	Image Doc. Displayed	PT
1	US 20020032323	☐

	L #	Hits	Search Text
1	L1	355	corynebacterium adj glutamicum
2	L2	0	sugar adj phsphotransferase$2
3	L4	0	l1 same l3
4	L3	4	sugar adj phosphotransferase$2
5	L5	8322	pyruvate
6	L6	2	l3 same l5
7	L7	413156	clon$3 or express$3 or recombinant
8	L8	1	l3 same l7
9	L9	0	pompejus.in.
10	L10	115	kroger.in.
11	L11	703	schroder.in.
12	L12	19	haberhauer.in.

	L #	Hits	Search Text
13	L13	836	l10 or l11 or l12
14	L14	0	l13 and l3
15	L15	0	l13 and l1